IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

I hereby certify that this paper is being In the Application of: Loughney deposited with the United States Postal Service in an envelope addressed to the Serial No. To be assigned Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Filed: Herewith Post Office Addressee" service of the United States Postal Service Under For: Phosphodiesterase 10 Mailing Label No. EK657826395US Group Art Unit: To be assigned Date: February 26, 2002 Examiner: To be assigned Richard Zimmermann

TRANSMITTAL OF SUBSTITUTE SEQUENCE LISTING

Assistant Commissioner for Patents Washington, DC 20231

Sir:

The Applicants respectfully request entry of the substitute Sequence Listing filed herewith. The substitute Sequence Listing corrects errors that were identified during the prosecution of the parent application (USSN 09/256,000) and is included at this time to expedite prosecution.

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821 and 1.825, are the same, and that the substitute Sequence Listing includes no new matter.

Respectfully submitted,

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Chicago, Illinois 60606-6357

(312) 474-6300

By

Joseph A. Williams, Jr. Registration No. 38,659

Attorney for Applicants

February 26, 2002

SEQUENCE LISTING

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170

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Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp 50

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val

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Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val 115

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- Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp 100 105 110
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tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc cc Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pr 10 15 20	g 164 O												
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg tt Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Ph 25 30 35	c 212 e												
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc tt Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Ph 40 45 50	c 260 e												
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga ga Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg As 55 60 65 7	Þ												
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta ca Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gli 75 80 85	g 356 1												
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu 90 95 100	g 404 1												
aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala 105 110 115	453												
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<213> Homo sapiens													

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Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala 20 25 30

Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu 35 40 45

Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro 50 55 60

Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp 65 70 75 80

Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala 85 90 95

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Asp Cys Ala 115

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<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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28

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

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90

95

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	gtc Val 100	Arg	tac Tyr	aat Asn	gac Asp	atc Ile 105	tca Ser	ccg Pro	ctg Leu	Glu	aac Asn 110	cac His	cac His	tgc Cys	gcc Ala	gtg Val 115	451
	gcc Ala	ttc Phe	cag Gln	atc Ile	ctc Leu 120	gcc Ala	gag Glu	cct Pro	gag Glu	tgc Cys 125	aac Asn	atc Ile	ttc Phe	tcc Ser	aac Asn 130	atc Ile	499
	cca Pro	cct Pro	gat Asp	999 Gly 135	ttc Phe	aag Lys	cag Gln	atc Ile	cga Arg 140	cag Gln	gga Gly	atg Met	atc Ile	aca Thr 145	tta Leu	atc Ile	547
	ttg Leu	gcc Ala	act Thr 150	gac Asp	atg Met	gca Ala	aga Arg	cat His 155	gca Ala	gaa Glu	att Ile	atg Met	gat Asp 160	tct Ser	ttc Phe	aaa Lys	595
	gag Glu	aaa Lys 165	atg Met	gag Glu	aat Asn	ttt Phe	gac Asp 170	tac Tyr	agc Ser	aac Asn	gag Glu	gag Glu 175	cac His	atg Met	acc Thr	ctg Leu	643
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	cca Pro	atg Met	gaa Glu	gtc Val	gca Ala 200	gag Glu	cct Pro	tgg Trp	gtg Val	gac Asp 205	tgt Cys	tta Leu	tta Leu	gag Glu	gaa Glu 210	tat Tyr	739
	ttt Phe	atg Met	cag Gln	agc Ser 215	gac Asp	cgt <b>Ar</b> g	gag Glu	aag Lys	tca Ser 220	gaa Glu	ggc Gly	ctt Leu	cct Pro	gtg Val 225	gca Ala	ccg Pro	787
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٠.	atc Ile	aag Lys 245	ttt Phe	gtc Val	ctg Leu	atc Ile	cca Pro 250	atg Met	ttt Phe	gaa Glu	aca Thr	gtg Val 255	acc Thr	aag Lys	ctc Leu	ttc Phe	883
	CCC Pro 260	atg Met	gtt Val	gag Glu	gag Glu	atc Ile 265	atg Met	ctg Leu	cag Gln	Pro	ctt Leu 270	tgg Trp	gaa Glu	tcc Ser	cga Arg	gat Asp 275	931
	cgc Arg	tac Tyr	gag Glu	gag Glu	ctg Leu 280	aag Lys	cgg Arg	ata Ile	gat Asp	gac Asp 285	gcc Ala	atg Met	aaa Lys	gag Glu	tta Leu 290	cag Gln	979
				gac Asp 295													1027

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 1070 Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala 310 315 320

ggggggggtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 1136

aagagetgee etgggeacet. ggeaceacaa gaceatgttt tetaagaace attttgttea 1196

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1303

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<211> 320

<212> PRT

<213> Homo sapiens

<400> 17

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Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn 20 25 30

Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala 35 40 45

Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe 50 60

Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp 65 70 75 80

Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr 85 90 95

Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His 100 105 110

Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe 115 120 125

Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile 130 135 140 Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp 145 150 155 160

Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn 180 185 190

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu 195 200 205

Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro

Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln 225 230 235 240

Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr 245 250 255

Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu 260 265 270

Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys 275 280 285

Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys 290 295 300

Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala 305 310 315 320

<210> 18

<211> 1887

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(1672)

<400> 18

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atc Ile	tac Tyr	ctg Leu 15	gac Asp	atc Ile	gat Asp	gga Gly	ege Arg 20	att Ile	cag Gln	aag Lys	gta Val	ato Ile 25	Phe	agc Ser	aag Lys	157
tac Tyr	tgc Cys 30	Asn	tcc Ser	agc Ser	gac Asp	atc Ile 35	atg Met	gac Asp	ctg Leu	ttc Phe	Cys 40	Ile	gcc Ala	acc	ggc	205
					acc Thr 50						Thr					253
					acc Thr											301
					gcc Ala											349
					gcg Ala											397
aaa Lys	atc Ile 110	aat Asn	gaa Glu	ctg Leu	aaa Lys	gct Ala 115	gaa Glu	gtt Val	gca Ala	aat Asn	cac His 120	ttg Leu	gct Ala	gtc Val	cta Leu	445
					ttg Leu 130											493
					aag Lys											541
					ccc Pro											589
	Leu				cgc Arg											637
		Glu			gag Glu											685
					gag Glu 210											733

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,													
							-1	9 -					
								Asn			agg Arg	781	
	 _		Сув	_		_	Tyr	_		Phe	cac His	829	
		His							tac Tyr 265		gtc Val	877	٠
	Cys								gat Asp			925	
									ccc Pro			973	
									gtc Val			1021	
_			_			His			gcc Ala	Gln		1069	
									cca Pro 345			1117	
	_								ttg Leu			1165	
									gag Glu			1213	
									ctg Leu			1261	
									cca Pro			1309	
					Cys				ttt Phe 425			1357	
				Glu				Ala	ttc Phe			1405	

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ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu 465 470 475	1501
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu 480 485 490	1549
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp 495 500 505	1597
agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat  Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp  510 515 520	1645
gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg Val Lys Asn Ser Glu Gly Asp Cys Ala 525 530	1692
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Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn 35 40 45	

- Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp 50 55 60
- Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro 65 70 75 80
- Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
- Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu 100 105 110
  - Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val 115 120 125
  - Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp 130 135 140
  - Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn 145 150 155 160
  - Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro 165 170 175
- Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr 180 185 190
- Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro 195 200 205
- Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu 210 215 220
- Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe 225 230 235 240
- Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His 245 250 255
- Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser 260 265 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala 275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln 290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro 305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro 325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile 340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His 355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr 370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys 385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys 420 425 430

Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr 435 440 445

Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met 450 455 460

Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu 465 470 475 480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile 485 490 495

Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser 500 505 510

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Glu Gly Asp Cys Ala 530

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<211> 1967

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Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu

ttg Leu	gaa Glu	gga Gly	cta Leu 180	aaa Lys	gtg Val	gtg Val	gag Glu	att Ile 185	gag Glu	aaa Lys	tgc Cys	aag Lys	agt Ser 190	gac Asp	att Ile	577
aag Lys	aag Lys	atg Met 195	agg Arg	gag Glu	gag Glu	ctg Leu	gcg Ala 200	gcc Ala	aga Arg	agc Ser	agc Ser	agg Arg 205	acc Thr	aac Asn	tgc Cys	625
ccc Pro	tgt Cys 210	aag Lys	tac Tyr	agt Ser	ttt Phe	ttg Leu 215	gat Asp	aac Asn	cac His	aag Lys	aag Lys 220	ttg Leu	act Thr	cct Pro	cga Arg	673
cgc Arg 225	gat, Asp	gtt Val	ccc Pro	act Thr	tac Tyr 230	ccc Pro	aag Lys	tac Tyr	ctg Leu	ctc Leu 235	tct Ser	cca Pro	gag Glu	acc Thr	atc Ile 240	721
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agg Arg	gac Asp	ttc Phe 275	agc Ser	atc Ile	aac Asn	cct Pro	gtc Val 280	acc Thr	ctc Leu	agg Arg	agg Arg	tgg Trp 285	ctg Leu	ttc Phe	tgc Cys	865
gtc Val	cac His 290	gac Asp	aac Asn	tac Tyr	aga Arg	aac Asn 295	aac Asn	ccc Pro	ttc Phe	cac His	aac Asn 300	ttc Phe	cgg Arg	cac His	tgc Cys	913
ttc Phe 305	tgc Cys	gtg Val	gcc Ala	cag Gln	atg Met 310	atg Met	tac Tyr	agc Ser	atg Met	gtc Val 315	tgg Trp	ctc Leu	tgc Cys	agt Ser	ctc Leu 320	961
cag Gln	gag Glu	aag Lys	ttc Phe	tca Ser 325	caa Gln	acg Thr	gat Asp	atc Ile	ctg Leu 330	atc Ile	cta Leu	atg Met	aca Thr	gcg Ala 335	gcc Ala	1009
atc	tgc Cys	cac His	gat Asp 340	ctg Leu	gac Asp	cat His	ccc Pro	ggc Gly 345	tac Tyr	aac Asn	aac Asn	acg Thr	tac Tyr 350	cag Gln	atc Ile	1057
aat Asn	gcc Ala	cgc Arg 355	aca Thr	gag Glu	ctg Leu	gcg Ala	gtc Val 360	cgc Arg	tac Tyr	aat Asn	gac Asp	atc Ile 365	tca Ser	ccg Pro	ctg Leu	1105
gag Glu	aac Asn 370	cac His	cac His	tgc Cys	Ala	gtg Val 375	gcc Ala	ttc Phe	cag Gln	atc Ile	ctc Leu 380	gcc Ala	gag Glu	cct Pro	gag Glu	1153
tgc Cys 385	aac Asn	atc Ile	ttc Phe	tcc Ser	aac Asn 390	atc Ile	cca Pro	cct Pro	gat Asp	ggg Gly 395	ttc Phe	aag Lys	cag Gln	atc Ile	cga Arg 400	1201

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cag Gln	gga Gly	atg Met	atc Il	aca Thr 405	tta Leu	atc Ile	ttg Leu	gcc Ala	act Thr 410	Asp	atg Met	gca Ala	aga Arg	cat His 415	gca Ala	1249
gaa Glu	att Ile	atg Met	gat Asp 420	tct Ser	ttc Phe	aaa Lys	gag Glu	aaa Lys 425	atg Met	gag Glu	aat Asn	ttt Phe	gac Asp 430	tac Tyr	agc Ser	1297
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gaa Glu	ggc Gly	ctt Leu	cct Pro	gtg Val 485	gca Ala	ccg Pro	ttc Phe	atg Met	gac Asp 490	cga Arg	gac Asp	aaa Lys	gtg Val	acc Thr 495	aag Lys	1489
gcc Ala	aca Thr	gcc Ala	cag Gln 500	att Ile	Gly ggg	ttc Phe	atc Ile	aag Lys 505	ttt Phe	gtc Val	ctg Leu	atc Ile	cca Pro 510	Met	ttt Phe	1537
gaa Glu	aca Thr	gtg Val 515	acc Thr	aag Lys	ctc Leu	ttc Phe	ccc Pro 520	atg Met	gtt Val	gag Glu	gag Glu	atc Ile 525	atg Met	ctg Leu	cag Gln	1585
cca Pro	ctt Leu 530	tgg Trp	gaa Glu	tcc Ser	cga Arg	gat Asp 535	cgc Arg	tac Tyr	gag Glu	gag Glu	ctg Leu 540	Lys	cgg Arg	ata Ile	gat Asp	1633
gac Asp 545	gcc Ala	atg Met	aaa Lys	gag Glu	tta Leu 550	cag Gln	aag Lys	aag Lys	act Thr	gac Asp 555	agc Ser	ttg Leu	acg Thr	tct Ser	260 G1Å aaa	1681
gcc Ala	acc Thr	gag Glu	aag Lys	tcc Ser 565	aga Arg	gag Glu	aga Arg	agc Ser	aga Arg 570	gat Asp	gtg Val	aaa Lys	aac Asn	agt Ser 575	gaa Glu	1729
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gaco	atgt	tť t	ctaa	gaac	c at	tttg	ttca	ctg	atac	aaa	aaaa	aaaa	aa g	gaat	tcatg	1901
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<211> 580

<212> PRT

<213> Homo sapiens

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Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg 85 90 95

Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser 100 105 110

Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu 115 120 125

Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu 130 135 140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu 145 150 155 160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile 180 185 190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys 195 200 205

Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210 215 220

Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile 225 230 235 240

3lu	Ala	Leu	Arg	Lys 245.	Pro	Thr	Phe	Asp	Val 250	Trp	Leu	Trp.	Glu	Pro 255	Asn
3lu	Met	Leu	Ser 260	Сув	Leu	Glu	His	Met 265	Tyr	His	Asp	Leu	Gly 270	Leu	Val
Arg	Asp	Phe 275	Ser	Ile	Asn	Pro	Val 280	Thr	Leu	Arg	Arg	Trp 285	Leu	Phe	Сув
Val	His 290	Asp	Asn	Tyr	Arg	Asn 295	Asn	Pro	Phe	His	Asn 300	Phe	Arg	His	Сув
Phe	Cys	Val	Ala	Gln	Met 310	Met	Tyr	Ser	Met	Val 315	Trp	Leu	Cys	Ser	Leu 320
Gln	Glu	Lys	Phe	Ser 325	Gln	Thr	Asp	Ile	Leu 330	Ile	Leu	Met	Thr	Ala 335	Ala
Ile	Cys	His	Asp 340	Leu	Asp	His	Pro	Gly 345	Tyr	Asn	Asn	Thr	Tyr 350	Gln	Ile
Asn		Arg 355	Thr	Glu	Leu	Ala	Val 360	Arg	Tyr	Asn	Asp	11e 365	Ser	Pro	Leu
	370					375				,	380		Glu		
385					390				-	395			Gln		400
				405					410				Arg	415	
	. •		420					425					Asp 430		
		435					440					445	Lys		
	450					455					460		Pro		
465				•	470					475			Glu		480
				485					490				Val	495	
			500					505				•	Pro 510		
		515					520	•				525	Met		
Pro	Leu 530	Trp	Glu	Ser	Arg	Asp 535	Arg	Tyr	Glu	Glu	Leu 540		Arg	Ile	Asp

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly 555 545 Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu 565 Gly Asp Cys Ala 580 <210> 22 <211> 1457 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (164) . . (1453) <400> 22 ggctcccggg cgtcccgggc ccggtggcgg cgcggctgtg gttggctgag cgccgcgggc 60 cgcccccgc ccgcccctc cctgctccc ctcccccgcc tcccgcggcg gctggcgtcg 120 ggaaagtaca gtaaaaagtc cgagtgcagc cgccgggcgc agg atg gga tcc ggc Met Gly Ser Gly . 1 tee tee age tac egg eee aag gee ate tac etg gae ate gat gga ege 223 Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg 10 att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271 Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met 30 319 gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser 40 ctg ctg acc acc gac gcc atg gtc tcc atc gac ccc acc atg ccc 367 Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro 415 geg aat tea gaa ege aet eeg tae aaa gtg aga eet gtg gee ate aag Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys **70** . 75 caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val

95

85

90

gca Ala	gag Glu	cag Gln	ttc Phe	tca Ser 105	Arg	gca Ala	ttc Phe	aaa Lys	Ile 110	Asn	gaa Glu	ctg Leu	aaa Lys	gct Ala 115	Glu	511
			cac His 120	Leu										Glu	gga Gly	559
			gtg Val													607
agg Arg	gag Glu 150	gag Glu	ctg Leu	gcg Ala	gcc Ala	aga Arg 155	agc Ser	agc Ser	agg Arg	acc Thr	aac Asn 160	tgc Cys	ccc Pro	tgt Cys	aag Lys	655
tac Tyr 165	agt Ser	ttt Phe	ttg Leu	gat Asp	aac Asn 170	cac His	aag Lys	aag Lys	ttg Leu	act Thr 175	cct Pro	cga Arg	cgc Arg	gat Asp	gtt Val 180	703
ccc Pro	act Thr	tac Tyr	ccc Pro	aag Lys 185	tac Tyr	ctg Leu	ctc Leu	tct Ser	cca Pro 190	gag Glu	acc Thr	atc Ile	gag Glu	gcc Ala 195	ctg Leu	751
			acc Thr 200											Met		799
			gag Glu													847
			cct Pro													895
			aac Asn													943
_	-	-	atg Met													991
			acg Thr 280													1039
			cat His													1087
		_	gcg Ala	-	_					Ser		Leu	-			1135

H	ac is 25	tgc Cys	gcc Ala	gtg Val	gcc Ala	ttc Phe 330	cag Gln	atc Ile	ctc Leu	gcc Ala	gag Glu 335	Pro	gag Glu	tgc Cys	aac Asn	atc Ile 340	1183
Þ	tc he	tcc Ser	aac Asn	atc Ile	cca Pro 345	cct Pro	gat Asp	Gly	ttc Phe	aag Lys 350	cag Gln	atc Ile	cga Arg	cag Gln	gga Gly 355		1231
a	tc	aca Thr	tta Leu	atc Ile 360	ttg Leu	gcc Ala	act Thr	gac Asp	atg Met 365	gca Ala	aga Arg	cat His	gca Ala	gaa Glu 370	att Ile	atg Met	1279
g A	at sp	tct Ser	ttc Phe 375	aaa Lys	gag Glu	aaa Lys	atg Met	gag Glu 380	aat Asn	ttt Phe	gac Asp	tac Tyr	agc Ser 385	aac Asn	gag Glu	gag Glu	1327
Н	ac is	atg Met 390	acc Thr	ctg Leu	ctg Leu	aag Lys	atg Met 395	att Ile	ttg Leu	ata Ile	aaa Lys	tgc Cys 400	tgt Cys	gat Asp	atc Ile	tct Ser	1375
A	ac sn 05	gag Glu	gtc Val	cgt Arg	cca Pro	atg Met 410	gaa Glu	gtc Val	gca Ala	gag Glu	cct Pro 415	tgg Trp	gtg Val	gac Asp	tgt Cys	tta Leu 420	1423
			gaa Glu								gaga	<b>a</b> .					1457
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S	er	Asp	Ile 35	Met	Asp	Leu	Phe	Cys 40	Ile	Ala	Thr	Gly	Leu 45	Pro	Arg	Asn	
T	hr	Thr 50	Ile	Ser	Leu	Leu	Thr 55	Thr	Asp	Asp	Ala	Met 60	Val	Ser	Ile	Asp	
	ro 65	Thr	Met	Pro	Ala	Asn 70	Ser	Glu	Arg	Thr	Pro 75	Tyr	Lys	Val	Arg	Pro 80	
V	al	Ala	Ile	Lys	Gln	Leu	Ser	Glu	Arg	Glu	Glu	Leu	Ile	Gln	Ser	Val	

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu 105 Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp 135 Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro 165 Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr 185 Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro 205 Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu 215 Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe 235 Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His 245 Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser 265 Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala 280 275 Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln 295 Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro 320 305 Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro 325 Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile 345 Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr 375 Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile L u Ile Lys Cys 390 400 385

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp 405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg 420 425 430

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<213> Artificial Sequence

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Asp Thr Lys Asp Asp Asp Lys

<210> 25

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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54

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<213> Artificial Sequence

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